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GENETIC DIVERGENCE FOR AGRO-MORPHOLOGICAL TRAITS IN FOXTAIL MILLET [*SETARIA ITALICA* (L.) BEAUV.]

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ABSTRACT
Thirty four Foxtail millet genotypes were evaluated for extent of Morphological diversity for twelve important quantitative traits using Mahalanobis D^2 statistics, in randomized block design with three replications. The genotypes exhibited highly significant differences for all the traits studied indicating sufficient genetic variability. The thirty four genotypes of foxtail millet were grouped into six clusters using Tocher's method. Cluster IV had maximum (6) genotypes. The genotypes in cluster IV and cluster VI due to maximum inter cluster distance (1604.09) between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme. The maximum contribution in the manifestation of genetic divergence was exhibited by inflorescence length (44.03 %) followed by flag leaf blade length (16.04 %), basal tillers number (10.34 %) and panicle exertion (9.98%) suggesting scope for improvement in these characters.

INTRODUCTION

Foxtail millet (*Setaria italica*) is thought to be native to southern Asia and is considered one of the oldest cultivated millets (Oelke *et al*., 1990). It is an introduced, annual, warm-season crop that grows 2–5 ft tall. The stems are course and leafy and more slender than those of pearl millet (Lee and Henning, 2014). It can form one or more tillering shoots (Dekker, 2003). The yellowish or purplish, nodding inflorescence is composed of a main stalk with many side branches. The seed heads are dense and bristly (Cash *et al.,* 2002) and the oval, convex seed grain can be a variety of colours. Foxtail millet grains are highly nutritious with good quality protein, rich in minerals, dietary fibre, phyto-chemicals and vitamins (Thiamin, Riboflavin, Niacin). Foxtail millet is similar to other warm-season grasses in terms of forage quality (Baltensperger, 1996). In India it is grown in semiarid regions of Bihar, Uttar Pradesh, Andhra Pradesh, Karnataka, Maharashtra, Tamil Nadu, Rajasthan and North Eastern states of our country (Jiayju, 1996). It is known for drought tolerant and grown well in where soil, climate and other conditions are less favourable. It possesses tolerance to pests and diseases. The potentiality of foxtail millet is not yet exploited properly in India. The yield levels in China is 11 t /ha, where as in India it is just ranging between 0.4-0.8t/ha suggesting a greater scope for exploitation of this millet under Indian conditions (Lakshmanan and Guggeri., 2001). The study of growth analysis would help in understanding contributions of various growth processes in accumulation of dry matter and yield .The low yield in foxtail millet is generally attributed to genetic, physiological and agronomic factors (Nirmalakumari and Vetriventhan, 2010). All the factors influencing growth and development of crop plants are to be integrated at an optimum level for maximum production potential in foxtail millet (Selvarani and Gomathinayagam , 2000).As reported by Deb (2009) maintaining crop diversity can ensure agricultural sustainability and food security. Precise information on the nature and degree of genetic diversity helps the plant breeder in choosing the diverse parents for purposeful hybridization. Several genetic diversity studies have been conducted on different crop species based on quantitative and qualitative traits in order to select genetically distant parents for hybridization (Shekhawat *et al*., 2001). In views of these facts, the present study was undertaken with the aim of examining the magnitude of genetic diversity and characters contributing to genetic diversity among foxtail genotypes for further utilization in breeding programme.

MATERIALS AND METHODS

The experiment was conducted in a randomized block design with three replications. The experimental materials were sown during kharif, 2014 keeping plot size 3.0 m x 2.5 m. In each replication each genotype was grown in a plot of 5 rows of 3 meter length each with a spacing of 22.5 cm between rows and 7.5 cm between plants (within rows). In order to compare the genotype unbiaselly, uniform plant population was kept in each row. Ten random plants per genotype per replication were tagged to record observations on yield and yield attributing traits *viz*. days to flowering, plant height (cm), basal tillers number, flag leaf blade length (mm), flag leaf blade width (mm), flag leaf sheath length (mm), peduncle length (mm),

panicle exertion (mm), inflorescence length (mm), inflorescence width (mm), weight of five panicles (g), yield per plot and yield (q/ha).

All the observations were calculated as per the descriptors of foxtail millet.

Basal tillers number was calculated by counting the number of basal tillers.

Flag leaf blade length was measured from ligule to leaf tip at the time of flowering while Flag leaf blade width was measured across the centre. Flag leaf sheath length was measured from node to ligule of flag leaf from the top at the time of flowering. Panicle exertion was measured as exertion of panicle at dough stage. Inflorescence length was measured from base to tip of longest spike on main tiller stage and inflorescence width was measured across the centre of longest finger at dough.

RESULTS AND DISCUSSION

The analysis of variance showed significant differences among all the genotypes for all the characters (Table 1). This exhibited the presence of considerable extent of variability among the genotypes which could be utilized in further breeding programme. These results are in agreement with the results obtained in foxtail millet by Gopalreddy *et al*. (2006) and Prasanna *et al*. (2013).

In the present investigation, thirty four genotypes were grouped into six clusters on the basis of D^2 statistics (Table 2). On the basis of inter or intra-cluster distance dendogram (Fig. 1) of thirty four foxtail millet genotypes were obtained. Cluster IV had maximum number of genotypes (9) *viz*. ISe 507, ISe 132, ISe 2, ISe302, ISe1820, ISe1563, ISe783, ISe1541, RAU 2, Cluster III had seven genotypes *viz*. ISe745, ISe114, ISe1736, ISe1745, ISe792, ISe1666, ISe1687. Cluster II had six genotypes *viz*. ISe983, ISe869, ISe 900, ISe 999, ISe 1892, ISe 963 while cluster V consisted of five genotypes namely ISe90, ISe375, ISe376, ISe1468, ISe1610,.Cluster I had four genotypes *viz*. ISe200,ISe907,ISe710,ISe1296 and cluster VI consisted of three genotypes namely, ISe1181, ISe 1665, ISe1234. The clustering pattern showed that genotypes of different geographical areas were clubbed in one group and also the genotypes of same geographical area were grouped into same cluster as well as in different cluster indicating that there was no formal relationship between geographical diversity and genetic diversity. Similar studied based on D^2 statistic was also performed by Arunkumar, (2013), Lakshmanan and Guggeri (2001), Selvarani and Gomathinayagam (2000).

Different clusters comprises unique feature for different resemblance between the genotypes presented in (Table 3). The genotypes in cluster IV and cluster VI due to maximum

Table 1 : Analysis of variance of thirty four genotypes of finger millet for twelve characters

Sl. no.	Source of variation characters	Mean sum of square due to Replication (d.f. = 2)	Treatment (d.f. = 33)	Error (d.f. = 66)
1	Days to Flowering	0.5588	97.8815**	1.9528
2	Plant Height (cm)	58.3635	1877.1470**	74.3835
3	Basal Tillers Number	0.0195	4.0689**	0.0907
4	Flag Leaf Blade Length (mm)	316.205	12702.7900**	129.5056
5	Flag Leaf Blade Width (mm)	19.5777	30.4578**	7.563
6	Flag Leaf Sheath Length (mm)	31.2889	1613.7329**	51.1439
7	Peduncle Length (mm)	50.3801	3429.3740**	97.1622
8	Panicle Exertion (mm)	38.2977	2979.0989**	37.4336
9	Inflorescence Length (mm)	37.6856	5786.0903**	41.7676
10	Inflorescence Width (mm)	18.4254	334.0157**	17.6688
11	Weight of five Panicles (g)	7.9624	249.6770**	12.7773
12	Yield (q/ha)	0.0513	50.4633**	3.6172

Table 2 : Clustering patterns of thirty four genotypes on the basis of D^2 statistics

Cluster No.	No. of Genotypes within cluster	Genotypes in cluster
I	4	ISe200, ISe907, ISe710, ISe1296
II	6	ISe983, ISe869, ISe900, ISe999, ISe1892, ISe963
III	7	ISe745, ISe114, ISe1736, ISe1745, ISe792, ISe1666, ISe1687,
IV	9	ISe507, ISe132, ISe2, ISe302, ISe1820, ISe1563, ISe783, ISe1541, RAU 2,
V	5	ISe90, ISe375, ISe376, ISe1468, ISe1610,
VI	3	ISe1181, ISe1665, ISe1234

Table 3 : Mean intra and inter-cluster distances among six clusters

Cluster No.	I	II	III	IV	IV	VI
I	111.415	322.394	489.993	285.686	599.249	1391.899
II		138.814	341.207	367.196	384.639	915.562
III			235.854	290.658	813.457	1477.820
IV				171.235	697.928	1604.090
V					252.343	636.234
VI						389.816

Table 4 : Cluster mean values of 6 clusters for different quantitative characters

Sl.No	ClustersCharacters	I	II	III	IV	V	VI
1	Days to Flowering	56.917	58.333	51.857	50.933	53.250	42.000
2	Plant Height (cm)	116.425	131.672	139.310	131.723	103.567	86.467
3	Basal Tillers Number	4.283	2.567	1.738	2.623	1.567	1.689
4	Flag Leaf Blade Length (mm)	314.908	354.917	400.129	401.637	327.100	234.722
5	Flag Leaf Blade Width (mm)	19.567	20.244	24.343	23.477	22.583	20.289
6	Flag Leaf Sheath Length (mm)	170.458	171.044	184.600	177.750	138.450	147.456
7	Peduncle Length (mm)	240.358	287.122	297.714	248.267	247.392	312.178
8	Panicle Exertion (mm)	73.208	115.111	113.086	73.623	115.450	166.711
9	Inflorescence Length (mm)	203.533	186.244	231.952	216.877	133.600	112.389
10	Inflorescence Width (mm)	44.833	43.811	45.976	52.470	54.575	42.778
11	Weight of five Panicles (g)	33.933	21.883	31.400	34.243	37.250	21.567
12	Yield (q/ha)	17.358	12.406	14.662	18.330	15.400	11.978

Table 5 : Per cent contribution towards divergence

Sl.no	Source	Times Ranked 1st	Contribution %
1	Days to Flowering	29	5.17
2	Plant Height (cm)	11	1.96
3	Basal Tillers Number	58	10.34
4	Flag Leaf Blade Length (mm)	90	16.04
5	Flag Leaf Blade Width (mm)	2	0.36
6	Flag Leaf Sheath Length (mm)	6	1.07
7	Peduncle Length (mm)	7	1.25
8	Panicle Exertion (mm)	56	9.98
9	Inflorescence Length (mm)	247	44.03
10	Inflorescence Width (mm)	10	1.78
11	Weight of five Panicles (g)	45	8.02
12	Yield (q/ha)	0	0.00

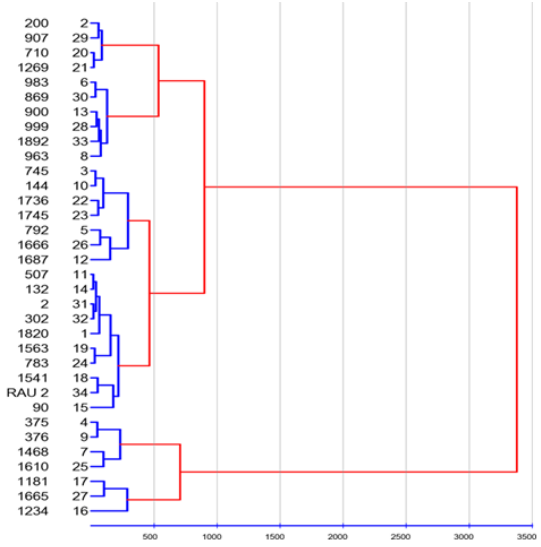

Figure1 : Ward's minimum variance dendrogram for distribution of thirty four genotypes in six cluster based on non-hierarchical Euclidean cluster analysis

inter cluster distance between them, exhibited high degree of genetic diversity and thus may be utilized under inter varietal hybridization programme (transgressive breeding) for getting high yielding recombinants. Similar inter varietal crosses may be attempted between genotypes in cluster III and VI and cluster I and IV. The lowest inter cluster distance was observed between cluster III and IV followed by cluster I and II and cluster II and III showing these clusters were relatively less divergent and crossing between them cannot produce vigorous offspring (F_1 progenies). Maximum intra cluster distance was observed in cluster VI followed by cluster IV, thus the genotypes within these cluster are more diverse with respect to each other. Further, genotypes present in the more distanced clusters will serve as good sources of divergent genes which is very much required for breeding to exploit heterosis as reported by Gill *et al*. (1995) or and to get good transgressive segregants in the segregating population.

In the present study, thirty four diverse genotypes were grouped into various cluster and suitable diverse genotypes were selected based on their cluster mean (Table 4). Cluster VI showed lowest mean value for days to flowering, plant height, basal tillers number, flag leaf blade length, inflorescence length, inflorescence width, weight of five panicle and yield and cluster I showed lowest mean value for peduncle length and panicle exertion. Cluster III showed highest mean value for plant height, flag leaf blade width, flag leaf blade width, inflorescence length. Cluster IV showed highest mean value for flag leaf blade length and yield. Cluster V showed highest mean value for inflorescence width and weight of five panicles. Cluster VI showed highest mean value for panicle length and panicle exertion. Cluster II showed highest mean value for days to flowering and cluster I showed highest mean value for basal number of tillers. Similar results were in agreement with Chidambaram and Palanisamy (1995), Dhembre and Kumar (2014), Gopal *et al*.(2006), Nirmalakumari and Vetriventhan (2010) and Prasanna *et al*. (2013).

The selection and choice of parents mainly depends upon contribution of characters towards divergence. The maximum contribution in the manifestation of genetic divergence was

exhibited by inflorescence length followed by flag leaf blade length, basal tillers number and panicle exertion suggesting scope for improvement in these characters. In other words, selection for these characters may be rewarding. Similar observation were recorded by Lakshmanan and Guggeri (2001) and Wolie *et al*. (2011).

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